FIG. 6A displays an alignment of a first portion of twenty-seven MSP polypeptides from *C. elegans*.

A2

FIG. 6B displays an alignment of the second portion of the twenty-seven MSP polypeptides from *C. elegans* shown in FIG. 6A. The SEQ ID Numbers are not meant to include the N-terminal most methionine which is believed to be cleaved during processing.

Please delete the paragraph beginning at page 17, line 12 with "There are likely ..."and ending on page 17, line 18 with "...into polypeptides" and replace with the following:

A3

There are likely more than sixty copies of the MSP gene in the *C. elegans* genome and it is believed that most of these MSP genes are transcribed. Referring to FIGS. 6A and 6B, twenty-seven MSP polypeptide sequences are provided corresponding to polypeptides transcribed from apparently distinct MSP genes or polynucleotide sequences. Certain other nematodes apparently have fewer copies of MSP. For example, *A. suum* are believed to have two copies of an MSP gene both of which are believed to be transcribed into polypeptides.

Please delete the paragraph beginning at page 17, line 19 with "Twenty-seven polypeptide..."and ending on page 18, line 3 with "...Stoye (1998)" and replace with the following:

A4

Twenty-seven polypeptide sequences for FIGS. 6A and 6B are aligned using Divide-and-Conquer Multiple Sequence Alignment which is currently available over the world wide web (www) at the URL http://bibiserv.techfak.uni-bielefeld.de/dca/. The server is located at the Practical Computer Science and Bioinformatics research group which is run by Robert Giegerich. The physical location is: Robert Giegerich, AG Praktische Informatik, Technische Fakultät, Universität Bielefeld, Postfach 10 01 31, D-33501 Bielefeld, Germany. The parameters used are Blosum 62 predefined substitution matrix, free shift activated, approximate cut positions activated, recursion stop size L set to 20, window size W set to 0, and weight intensity lambda set to 0. The algorithm and method are disclosed in Stoye (1998).

Please delete the paragraph beginning at page 18, line 4 with "Referring to ..."and ending on page 18, line 9 with "...as shown in FIG. 6" and replace with the following:

Referring to FIGS. 6A and 6B, it is known that the N-terminal most methionine (from the ATG translation start site) is cleaved. It is expected that both forms (with and without the methionine) of MSP polypeptides are active in FSM; therefore, the methionine was included in FIG. 6A. However, the references to the SEQ ID Numbers provided in FIG. 6B correspond to MSP polypeptide sequences of 126 amino acids and are without each N-terminal most methionine as shown in FIG. 6A.

Please delete the paragraph beginning at page 18, line 10 with "Again, referring..."and ending on page 18, line 23 with "...as a percent" and replace with the following:

A4 Cont.

Again, referring to FIGS. 6A and 6B, the sequences of the numerous *C. elegans* MSP display a high degree of sequence homology. Very few sequence variations are observed. Residues that vary from the global (general) consensus within a column (determined visually) are marked in bold letter and underlined in FIGS. 6A and 6B. Because MSP polypeptide sequences, and even those of the most divergent known nematodes (see below), are so highly conserved; the preferred method for alignment is by visual inspection. For example, two or more MSP polypeptide sequences can be easily lined up next to one another on a computer screen or as written out on a paper and one moved against another until the majority of the bases match. Percent identity between any two sequences is calculated by counting the number of residues that do not match, dividing by the total number of residues in the total sequence being compared (or the shortest of the sequences being compared if one of the pair is shorter in length), multiplying by 100, and expressing the resulting value as a percent.

Please delete the paragraph beginning at page 49, line 24 with "Recombinant MSP..."and ending on page 50, line 12 with "...known in the art" and replace with the following:

A5

Recombinant MSP bacterial strains were produced by cloning MSP-142 and MSP-38 into the pQe-30 6-His vector from Qiagen. Primers specific for MSP were made that contained a 5' BamHI site (5' primer) or a 5' HindIII (3' primer) followed by the respective MSP-coding sequences. MSP-38 and MSP-142 were amplified by PCR, cut with BamHI and HindIII, and ligated into the pQe-30 vector (FIGS. 6A and 6B) which was also cut with BamHI and HindIII. This strategy generated a vector containing an IPTG-inducible promoter followed by an initiator methionine, an N-terminal 6-His tag, and the respective MSP-38 or MSP-142 coding sequences. This construct was then transformed into M15(pREP4) bacterial cells and vector-containing colonies were selected with LB medium containing Ampicillin and Kanamycin. MSP-containing colonies were grown overnight and then MSP expression was induced for 4 hours with 1 mM IPTG. Induced bacteria were pelleted, lysed, and purified using a NiNTA agarose column, which binds the 6-His tag. 6-His purification is known in the art.

In the Claims

Cancel claims 1-33 and 40-45.